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1005

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/950,071

DATE: 10/04/2001

TIME: 10:31:45

Input Set : A:\212532US0.txt

Output Set: N:\CRF3\10042001\I950071.raw

ENTERED

3 <110> APPLICANT: FARWICK, Mike
 4 HUTHMACHER, Klaus
 5 PFEFFERLE, Walter
 6 BATHE, Brigitte
 8 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE RODA PROTEIN
 10 <130> FILE REFERENCE: 212532US0
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/950,071
 C--> 12 <141> CURRENT FILING DATE: 2001-09-12
 12 <150> PRIOR APPLICATION NUMBER: DE10044943.3
 13 <151> PRIOR FILING DATE: 2000-09-12
 15 <150> PRIOR APPLICATION NUMBER: DE10132947.4
 16 <151> PRIOR FILING DATE: 2001-07-06
 18 <160> NUMBER OF SEQ ID NOS: 4
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1761
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Corynebacterium glutamicum
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (238)..(1560)
 30 <223> OTHER INFORMATION:
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 38 cgaggtccag gcgcaaattgc aacggctggc tgctcaagct ttgccagtgt gcgtgaactt 180
 40 agaagtaaca accggtggcg atagaaacga acccgagtc aattgtaggg aggtctc 237
 42 atg aac acg ctt gaa cga tta aag ctt cgt cgc acg gaa atg tgg ctg 285
 43 Met Asn Thr Leu Glu Arg Leu Lys Leu Arg Arg Thr Glu Met Trp Leu
 44 1 5 10 15
 46 ctg ata ctt gcc aca ctc gtt gtg tgc atc atg ttc atc agc ctc gag 333
 47 Leu Ile Leu Ala Thr Leu Val Val Ser Ile Met Phe Ile Ser Leu Glu
 48 20 25 30
 50 ctg gcc atg ggc aat gag ttg ggt acc cat att ttg atg ctg atg ggc 381
 51 Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly
 52 35 40 45
 54 gga tat atc ggt atc ttc atc gtc gcg cac cta gcc atg gca tgg gtg 429
 55 Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val
 56 50 55 60
 58 gcg ccg ttt gct gat caa atc atg ctg cct gtg gtg gcg gtg ctc aat 477
 59 Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn
 60 65 70 75 80
 62 ggc att ggt ttg gtg atg att tat cgc ctt gat gag gcc acg ggc tac 525
 63 Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr
 64 85 90 95
 66 agc acg gtc aat agc caa ttg atg tgg acg gtt gtt ggc gtc acg ctg 573
 67 Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu

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68	100	105	110	
70 atg gtg gct gtg ttg ttg ctg ttg cgt gat tac aag tcg ctt tcg cgt				621
71 Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg				
72	115	120	125	
74 tat tcc tac ctc ctc ggt gtg gtg ggc atc gtg ctg ctg gcg ctg cct				669
75 Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro				
76	130	135	140	
78 ctc gtg tgg ccg cag cca ggc ggc gtg gaa gcc cgc atc tgg att tgg				717
79 Leu Val Trp Pro Gln Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp				
80	145	150	155	160
82 ctt gga cct ttc tcc atc cag cca ggt gag ttc tcc aag att ttg ctg				765
83 Leu Gly Pro Phe Ser Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu				
84	165	170	175	
86 ctg ctg ttc ttt gct cag ctg cta gcc acc aag cgt gct ttg ttt act				813
87 Leu Leu Phe Phe Ala Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr				
88	180	185	190	
90 gtt gcg ggc tac cgt ttc ctc ggc atg gat ttc cct cgt ttg cgt gac				861
91 Val Ala Gly Tyr Arg Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp				
92	195	200	205	
94 ctc gcg ccg att ctt gtg gtg tgg gcg ttg gct att ttg atc atg gct				909
95 Leu Ala Pro Ile Leu Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala				
96	210	215	220	
98 ggc gcc aac gac ttc ggt cct gca ctg ctg ctt ttc act acc gtt ttg				957
99 Gly Ala Asn Asp Phe Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu				
100	225	230	235	240
102 gcc atg gtg tac ctg gct acc ggc cgt ggt tcc tgg ctg ttg att ggt				1005
103 Ala Met Val Tyr Leu Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly				
104	245	250	255	
106 gct gtg ttg gtg gct gtc ggc gcg ttc gcg gtg tac caa gtt tca agc				1053
107 Ala Val Leu Val Ala Val Gly Ala Phe Ala Val Tyr Gln Val Ser Ser				
108	260	265	270	
110 aag att cag gaa cgc gtg caa aac ttc gtg gat cct gtg gcc cac tat				1101
111 Lys Ile Gln Glu Arg Val Gln Asn Phe Val Asp Pro Val Ala His Tyr				
112	275	280	285	
114 gac acc acc ggt tac cag ctg tcc cag tcc ttg ttt ggc atg agt tgg				1149
115 Asp Thr Thr Gly Tyr Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp				
116	290	295	300	
118 ggc gga atc acc ggc acc ggc att ggt cag ggt tac ccc aac atg atc				1197
119 Gly Gly Ile Thr Gly Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile				
120	305	310	315	320
122 cct gtc gtg cac tcg gac ttc att ctc gca gcc att ggt gag gag ctt				1245
123 Pro Val Val His Ser Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu				
124	325	330	335	
126 ggt ctg att ggc ctg gcg gcc atc atc gtg ctg ttt ggt gtg ttt gtc				1293
127 Gly Leu Ile Gly Leu Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val				
128	340	345	350	
130 acc cgc ggt atg cgc acc gct acc ctg gct cgt gac agc tac gga aag				1341
131 Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys				
132	355	360	365	

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134 ctc gtg gca tct ggt ctg tcg atg acc atc atg atc cag att ttc gtc      1389
135 Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val
136      370      375      380
138 gtc gtg gca ggt att tct tca ctg atg ccc atg aca ggt ttg acc act      1437
139 Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr
140 385      390      395      400
142 ccg ttt atg tcc cag ggt ggt tca tcc ctg atg gct aac tac att ctg      1485
143 Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu
144      405      410      415
146 atg gcc atc atc ttg cgt att tct gac agt gcc cgc cga cct gtc atg      1533
147 Met Ala Ile Ile Leu Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met
148      420      425      430
150 tcc aag caa gca tcg gag gtg gct gcg tgaaccgctc gattcgaatc      1580
151 Ser Lys Gln Ala Ser Glu Val Ala Ala
152      435      440
154 acatccctct tctcttttgc tctgatcttg gtgctcgtag caaacctcac ctggattcag      1640
156 gcttttaggg acgatgatct tgctcagaac ccactgaacg cacgtggttt cctggaggcg      1700
158 aagtccactc cgcgtggaca gatttcaact ggtggccaag tactcgcaga gtcctccag      1760
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164 <211> LENGTH: 441
165 <212> TYPE: PRT
166 <213> ORGANISM: Corynebacterium glutamicum
168 <400> SEQUENCE: 2
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175      20      25      30
178 Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly
179      35      40      45
182 Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val
183      50      55      60
186 Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn
187 65      70      75      80
190 Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr
191      85      90      95
194 Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu
195      100      105      110
198 Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg
199      115      120      125
202 Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Ala Leu Pro
203      130      135      140
206 Leu Val Trp Pro Gln Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp
207 145      150      155      160
210 Leu Gly Pro Phe Ser Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu
211      165      170      175
214 Leu Leu Phe Phe Ala Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr
215      180      185      190
218 Val Ala Gly Tyr Arg Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp

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219      195      200      205
222 Leu Ala Pro Ile Leu Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala
223      210      215      220
226 Gly Ala Asn Asp Phe Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu
227 225      230      235      240
230 Ala Met Val Tyr Leu Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly
231      245      250      255
234 Ala Val Leu Val Ala Val Gly Ala Phe Ala Val Tyr Gln Val Ser Ser
235      260      265      270
238 Lys Ile Gln Glu Arg Val Gln Asn Phe Val Asp Pro Val Ala His Tyr
239      275      280      285
242 Asp Thr Thr Gly Tyr Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp
243      290      295      300
246 Gly Gly Ile Thr Gly Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile
247 305      310      315      320
250 Pro Val Val His Ser Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu
251      325      330      335
254 Gly Leu Ile Gly Leu Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val
255      340      345      350
258 Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys
259      355      360      365
262 Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val
263      370      375      380
266 Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr
267 385      390      395      400
270 Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu
271      405      410      415
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275      420      425      430
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279      435      440
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285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
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297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: synthetic DNA
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VERIFICATION SUMMARY

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DATE: 10/04/2001

TIME: 10:31:46

Input Set : A:\212532US0.txt

Output Set: N:\CRF3\10042001\I950071.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date